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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2009; month=6; day=26; hr=9; min=43; sec=18; ms=727;]

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Application No: 10554625 Version No: 1.0

Input Set:

Output Set:

Started: 2009-06-11 15:50:53.475
Finished: 2009-06-11 15:50:54.066
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 591 ms
Total Warnings: 2
Total Errors: 18
No. of SeqIDs Defined: 2
Actual SeqID Count: 2

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (2)

SEQUENCE LISTING

<110> CHIRON CORPORATION

<120> COMPOSITIONS COMPRISING CATIONIC MICROPARTICLES
AND HCV E1E2 DNA AND METHODS OF USE THEREOF

<130> 2300-20407.40 (PP20407.003)

<140> 10554625

<141> 2009-06-11

<150> PCT/US2004/012510

<151> 2004-04-23

<150> 60/465,841

<151> 2003-04-25

<160> 2

<170> PatentIn Ver. 2.0

<210> 1

<211> 1914

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: HCV-1 E1/E2/p7 region

<220>

<221> CDS

<222> (1)..(1911)

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1 5 10 15

gct tcg gcc tac caa gtg cgc aac tcc acg ggg ctc tac cac gtc acc 96
Ala Ser Ala Tyr Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr
20 25 30

aat gat tgc cct aac tcg agt att gtg tac gag gcg gcc gat gcc atc 144
Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Ala Ile
35 40 45

ctg cac act ccg ggg tgc gtc cct tgc gtt cgc gag ggc aac gcc tcg 192
Leu His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ala Ser
50 55 60

agg tgt tgg gtg gcg atg acc cct acg gtg gcc acc agg gat ggc aaa 240
Arg Cys Trp Val Ala Met Thr Pro Thr Val Ala Thr Arg Asp Gly Lys
65 70 75 80

ctc ccc gcg acg cag ctt cga cgt cac atc gat ctg ctt gtc ggg agc 288

Leu	Pro	Ala	Thr	Gln	Leu	Arg	Arg	His	Ile	Asp	Leu	Leu	Val	Gly	Ser	
85					90						95					
gcc acc ctc tgt tcg gcc ctc tac gtg ggg gac ctg tgc ggg tct gtc															336	
Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Leu	Cys	Gly	Ser	Val	
100					105						110					
ttt ctt gtc ggc caa ctg ttt acc ttc tct ccc agg cgc cac tgg acg															384	
Phe	Leu	Val	Gly	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg	Arg	His	Trp	Thr	
115					120						125					
acg caa ggt tgc aat tgc tct atc tat ccc ggc cat ata acg ggt cac															432	
Thr	Gln	Gly	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His	Ile	Thr	Gly	His	
130					135						140					
cgc atg gca tgg gat atg atg atg aac tgg tcc cct acg acg gcg ttg															480	
Arg	Met	Ala	Trp	Asp	Met	Met	Asn	Trp	Ser	Pro	Thr	Thr	Ala	Leu		
145					150						155			160		
gta atg gct cag ctg ctc cgg atc cca caa gcc atc ttg gac atg atc															528	
Val	Met	Ala	Gln	Leu	Leu	Arg	Ile	Pro	Gln	Ala	Ile	Leu	Asp	Met	Ile	
165					170						175					
gct ggt gct cac tgg gga gtc ctg gcg ggc ata gcg tat ttc tcc atg															576	
Ala	Gly	Ala	His	Trp	Gly	Val	Leu	Ala	Gly	Ile	Ala	Tyr	Phe	Ser	Met	
180					185						190					
gtg ggg aac tgg gcg aag gtc ctg gta gtg ctg cta ttt gcc ggc															624	
Val	Gly	Asn	Trp	Ala	Lys	Val	Leu	Val	Val	Leu	Leu	Leu	Phe	Ala	Gly	
195					200						205					
gtc gac gcg gaa acc cac gtc acc ggg gga agt gcc ggc cac act gtg															672	
Val	Asp	Ala	Glu	Thr	His	Val	Thr	Gly	Gly	Ser	Ala	Gly	His	Thr	Val	
210					215						220					
tct gga ttt gtt agc ctc ctc gca cca ggc gcc aag cag aac gtc cag															720	
Ser	Gly	Phe	Val	Ser	Leu	Leu	Ala	Pro	Gly	Ala	Lys	Gln	Asn	Val	Gln	
225					230						235			240		
ctg atc aac acc aac ggc agt tgg cac ctc aat agc acg gcc ctg aac															768	
Leu	Ile	Asn	Thr	Asn	Gly	Ser	Trp	His	Leu	Asn	Ser	Thr	Ala	Leu	Asn	
245					250						255					
tgc aat gat agc ctc aac acc ggc tgg ttg gca ggg ctt ttc tat cac															816	
Cys	Asn	Asp	Ser	Leu	Asn	Thr	Gly	Trp	Leu	Ala	Gly	Leu	Phe	Tyr	His	
260					265						270					
cac aag ttc aac tct tca ggc tgt cct gag agg cta gcc agc tgc cga															864	
His	Lys	Phe	Asn	Ser	Ser	Gly	Cys	Pro	Glu	Arg	Leu	Ala	Ser	Cys	Arg	
275					280						285					
ccc ctt acc gat ttt gac cag ggc tgg ggc cct atc agt tat gcc aac															912	
Pro	Leu	Thr	Asp	Phe	Asp	Gln	Gly	Trp	Gly	Pro	Ile	Ser	Tyr	Ala	Asn	
290					295						300					
gga agc ggc ccc gac cag cgc ccc tac tgc tgg cac tac ccc cca aaa															960	

Gly Ser Gly Pro Asp Gln Arg Pro Tyr Cys Trp His Tyr Pro Pro Lys				
305	310	315	320	
cct tgc ggt att gtg ccc gcg aag agt gtg tgt ggt ccg gta tat tgc				1008
Pro Cys Gly Ile Val Pro Ala Lys Ser Val Cys Gly Pro Val Tyr Cys				
325	330	335		
ttc act ccc agc ccc gtg gtg gga acg acc gac agg tcg ggc gcg				1056
Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Ser Gly Ala				
340	345	350		
ccc acc tac agc tgg ggt gaa aat gat acg gac gtc ttc gtc ctt aac				1104
Pro Thr Tyr Ser Trp Gly Glu Asn Asp Thr Asp Val Phe Val Leu Asn				
355	360	365		
aat acc agg cca ccg ctg ggc aat tgg ttc ggt tgt acc tgg atg aac				1152
Asn Thr Arg Pro Pro Leu Gly Asn Trp Phe Gly Cys Thr Trp Met Asn				
370	375	380		
tca act gga ttc acc aaa gtg tgc gga gcg cct cct tgt gtc atc gga				1200
Ser Thr Gly Phe Thr Lys Val Cys Gly Ala Pro Pro Cys Val Ile Gly				
385	390	395	400	
ggg gcg ggc aac aac acc ctg cac tgc ccc act gat tgc ttc cgc aag				1248
Gly Ala Gly Asn Asn Thr Leu His Cys Pro Thr Asp Cys Phe Arg Lys				
405	410	415		
cat ccg gac gcc aca tac tct cgg tgc ggc tcc ggt ccc tgg atc aca				1296
His Pro Asp Ala Thr Tyr Ser Arg Cys Gly Ser Gly Pro Trp Ile Thr				
420	425	430		
ccc agg tgc ctg gtc gac tac ccg tat agg ctt tgg cat tat cct tgt				1344
Pro Arg Cys Leu Val Asp Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys				
435	440	445		
acc atc aac tac act ata ttt aaa atc agg atg tac gtg gga ggg gtc				1392
Thr Ile Asn Tyr Thr Ile Phe Lys Ile Arg Met Tyr Val Gly Gly Val				
450	455	460		
gag cac agg ctg gaa gct gcc tgc aac tgg acg cgg ggc gaa cgt tgc				1440
Glu His Arg Leu Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys				
465	470	475	480	
gat ctg gaa gat agg gac agg tcc gag ctc acg ccg tta ctg ctg acc				1488
Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Thr				
485	490	495		
act aca cag tgg cag gtc ctc ccg tgt tcc ttc aca acc ctg cca gcc				1536
Thr Thr Gln Trp Gln Val Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala				
500	505	510		
ttg tcc acc ggc ctc atc cac ctc cac cag aac att gtg gac gtg cag				1584
Leu Ser Thr Gly Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln				
515	520	525		
tac ttg tac ggg gtg ggg tca agc atc gcg tcc tgg gcc att aag tgg				1632
Tyr Leu Tyr Gly Val Gly Ser Ser Ile Ala Ser Trp Ala Ile Lys Trp				

530	535	540	
gag tac gtc gtc ctc ctg ttc ctt ctg ctt gca gac gcg ggc gtc tgc Glu Tyr Val Val Leu Leu Phe Leu Leu Ala Asp Ala Arg Val Cys			1680
545	550	555	560
tcc tgc ttg tgg atg atg cta ctc ata tcc caa gcg gaa gcg gct ttg Ser Cys Leu Trp Met Met Leu Leu Ile Ser Gln Ala Glu Ala Ala Leu			1728
565	570	575	
gag aac ctc gta ata ctt aat gca gca tcc ctg gcc ggg acg cac ggt Glu Asn Leu Val Ile Leu Asn Ala Ala Ser Leu Ala Gly Thr His Gly			1776
580	585	590	
ctt gta tcc ttc ctc gtg ttc ttc tgc ttt gca tgg tat ctg aag ggt Leu Val Ser Phe Leu Val Phe Phe Cys Phe Ala Trp Tyr Leu Lys Gly			1824
595	600	605	
aag tgg gtg ccc gga gcg gtc tac acc ttc tac ggg atg tgg cct ctc Lys Trp Val Pro Gly Ala Val Tyr Thr Phe Tyr Gly Met Trp Pro Leu			1872
610	615	620	
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<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence: HCV-1 E1/E2/p7 region			
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Ala Ser Ala Tyr Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr			
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Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Ala Ile			
35	40	45	
Leu His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ala Ser			
50	55	60	
Arg Cys Trp Val Ala Met Thr Pro Thr Val Ala Thr Arg Asp Gly Lys			
65	70	75	80
Leu Pro Ala Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val Gly Ser			
85	90	95	
Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Ser Val			
100	105	110	

Phe Leu Val Gly Gln Leu Phe Thr Phe Ser Pro Arg Arg His Trp Thr
115 120 125

Thr Gln Gly Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His
130 135 140

Arg Met Ala Trp Asp Met Met Asn Trp Ser Pro Thr Thr Ala Leu
145 150 155 160

Val Met Ala Gln Leu Leu Arg Ile Pro Gln Ala Ile Leu Asp Met Ile
165 170 175

Ala Gly Ala His Trp Gly Val Leu Ala Gly Ile Ala Tyr Phe Ser Met
180 185 190

Val Gly Asn Trp Ala Lys Val Leu Val Val Leu Leu Phe Ala Gly
195 200 205

Val Asp Ala Glu Thr His Val Thr Gly Gly Ser Ala Gly His Thr Val
210 215 220

Ser Gly Phe Val Ser Leu Leu Ala Pro Gly Ala Lys Gln Asn Val Gln
225 230 235 240

Leu Ile Asn Thr Asn Gly Ser Trp His Leu Asn Ser Thr Ala Leu Asn
245 250 255

Cys Asn Asp Ser Leu Asn Thr Gly Trp Leu Ala Gly Leu Phe Tyr His
260 265 270

His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg
275 280 285

Pro Leu Thr Asp Phe Asp Gln Gly Trp Gly Pro Ile Ser Tyr Ala Asn
290 295 300

Gly Ser Gly Pro Asp Gln Arg Pro Tyr Cys Trp His Tyr Pro Pro Lys
305 310 315 320

Pro Cys Gly Ile Val Pro Ala Lys Ser Val Cys Gly Pro Val Tyr Cys
325 330 335

Phe Thr Pro Ser Pro Val Val Gly Thr Thr Asp Arg Ser Gly Ala
340 345 350

Pro Thr Tyr Ser Trp Gly Glu Asn Asp Thr Asp Val Phe Val Leu Asn
355 360 365

Asn Thr Arg Pro Pro Leu Gly Asn Trp Phe Gly Cys Thr Trp Met Asn
370 375 380

Ser Thr Gly Phe Thr Lys Val Cys Gly Ala Pro Pro Cys Val Ile Gly
385 390 395 400

Gly Ala Gly Asn Asn Thr Leu His Cys Pro Thr Asp Cys Phe Arg Lys
405 410 415

His Pro Asp Ala Thr Tyr Ser Arg Cys Gly Ser Gly Pro Trp Ile Thr
420 425 430

Pro Arg Cys Leu Val Asp Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys
435 440 445

Thr Ile Asn Tyr Thr Ile Phe Lys Ile Arg Met Tyr Val Gly Gly Val
450 455 460

Glu His Arg Leu Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys
465 470 475 480

Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Thr
485 490 495

Thr Thr Gln Trp Gln Val Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala
500 505 510

Leu Ser Thr Gly Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln
515 520 525

Tyr Leu Tyr Gly Val Gly Ser Ser Ile Ala Ser Trp Ala Ile Lys Trp
530 535 540

Glu Tyr Val Val Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Val Cys
545 550 555 560

Ser Cys Leu Trp Met Met Leu Leu Ile Ser Gln Ala Glu Ala Ala Leu
565 570 575

Glu Asn Leu Val Ile Leu Asn Ala Ala Ser Leu Ala Gly Thr His Gly
580 585 590

Leu Val Ser Phe Leu Val Phe Phe Cys Phe Ala Trp Tyr Leu Lys Gly
595 600 605

Lys Trp Val Pro Gly Ala Val Tyr Thr Phe Tyr Gly Met Trp Pro Leu
610 615 620

Leu Leu Leu Leu Ala Leu Pro Gln Arg Ala Tyr Ala
625 630 635